EXHIBIT 1: Alignment of Xenopus APC (Query) with Murine APC (Subject)

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> sp|Q61315|APC_MOUSE G Adenomatous polyposis coli protein (Protein APC)
(mAPC)
 gb|AAB59632.1| UG APC
Length=2845

 Score = 1357 bits (3512),  Expect = 0.0, Method: Composition-based stats.
 Identities = 742/861 (86%), Positives = 790/861 (91%), Gaps = 8/861 (0%)

Query  1    MAAASYDQLVKQVEALTMENTNLRQELEDNSNHLTKLETEATNMKEVLKQLQGSIEDEAM  60
            MAAASYDQL+KQVEAL MEN+NLRQELEDNSNHLTKLETEA+NMKEVLKQLQGSIEDE M
Sbjct  1    MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDETM  60

Query  61   ASSGPIDLLERFKDLNLDSSNIPAGKARPKMSMRSYGSREGSLSGHSGECSPVPVGSFQR  120
            +SG IDLLER K+ NLDS N P  K R KMS+RSYGSREGS+S  SGECSPVP+GSF R
Sbjct  61   -TSGQIDLLERLKEFNLDS-NFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR  118

Query  121  RGLLNGSRESAGYMEELEKERLLLIAEHEKEEKEKRWYYAQLQNLTKRIDSLPLTENFSM  180
            R  +NGSRES GY+EELEKER LL+A+ +KEEKEK WYYAQLQNLTKRIDSLPLTENFS+
Sbjct  119  RTFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL  178

Query  181  QTDMTRRQLEYEARQIRAAMEEQLGTCQDMEKRVQTRVGKIHQIEEEILRIRQLLQSQVA  240
            QTDMTRRQLEYEARQIRAAMEEQLGTCQDMEKR Q R+ +I QIE++ILR+RQLLQSQ A
Sbjct  179  QTDMTRRQLEYEARQIRAAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRVRQLLQSQAA  238

Query  241  EAAERTPQSKHDAGSRDAEKLPDGQGTSEITASGNVGSGQGSSSRADHDTTSVMSSNSTY  300
            EA ER+ QS+HDA S +A +  +G G +E   + +  SGQ  ++R DH+T SV+SS+ T+
Sbjct  239  EA-ERSSQSRHDAASHEAGRQHEGHGVAESNTAAS-SSGQSPATRVDHETASVLSSSGTH  296

Query  301  SVPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCIAMRQSGCLPLLIQ  360
            S PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCI+MRQSGCLPLLIQ
Sbjct  297  SAPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQ  356

Query  361  LLHGNDKDSVLLGNSRGSKEARASGSAALDNIIHSQPDDKRGRREIRVLHLLEQIRAYCE  420
            LLHGNDKDSVLLGNSRGSKEARA  SAAL NIIHSQPDDKRGRREIRVLHLLEQIRAYCE
Sbjct  357  LLHGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCE  416

Query  421  TCWEWQEAHEQGMDQDKNPMPAPVDHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAEL  480
            TCWEWQEAHEQGMDQDKNPMPAPV+HQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAEL
Sbjct  417  TCWEWQEAHEQGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAEL  476

Query  481  LQVDCEMYGLINDHYSVTLRRYAGMALTNLTFGDVANKATLCSMKSCMRALVAQLKSESE  540
            LQVDCEMYGL NDHYSVTLRRYAGMALTNLTFGDVANKATLCSMK CMRALVAQLKSESE
Sbjct  477  LQVDCEMYGLTNDHYSVTLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESE  536

Query  541  DLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALDVKKESTLKSVLSALWNLSAH  600
            DLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECAL+VKKESTLKSVLSALWNLSAH
Sbjct  537  DLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAH  596
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Query  601  CTENKADICSVDGALAFLVSTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRE  660
            CTENKADIC+VDGALAFLV TLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRE
Sbjct  597  CTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRE  656

Query  661  NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNAKDQEGLWDMGAVSMLKNLIHSKHKMI  720
            NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARN KDQE LWDMGAVSMLKNLIHSKHKMI
Sbjct  657  NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKMI  716

Query  721  AMGSAAALRNLMANRPAKYKDANIMSPGSSVPSLHVRKQKALEAELDAQHLSETFDNIDN  780
            AMGSAAALRNLMANRPAKYKDANIMSPGSS+PSLHVRKQKALEAELDAQHLSETFDNIDN
Sbjct  717  AMGSAAALRNLMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDN  776

Query  781  LSPKTTHRNKQRHKQNLCSEYALDSSRHDDSICRSDNFSIGNLTVLSPYINTTVLPGSSS  840
            LSPK +HR+KQRHKQNL  +YA D++RHDDS  RSDNF+ GN+TVLSPY+NTTVLP SSS
Sbjct  777  LSPKASHRSKQRHKQNLYGDYAFDANRHDDS-+RSDNFNTGNMTVLSPYLNTTVLPSSSS  834

Query  841  PRPTMDGSRPEKDR--ERTAG   859
             R ++D SR EKDR  ER  G
Sbjct  835  SRGSLDSSRSEKDRSLERERG   855
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